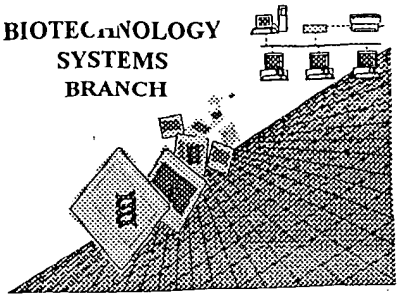
0400
03/08/0

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/779,050

Source: OIPE

Date Processed by STIC: 3/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/779,050

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ✓ Variable Length
Sequence(s) 5 (maybe more) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING DATE: 03/07/2001
PATENT APPLICATION: US/09/779,050 TIME: 11:03:02

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

Does Not Comply
Corrected Diskette Needed

p 6

```
  3 <110> APPLICANT: BOYLE, WILLIAM
  4       HSU, HAILING
  6 <120> TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
  8 <130> FILE REFERENCE: A-570B
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/779,050
 11 <141> CURRENT FILING DATE: 2001-02-12
 13 <150> PRIOR APPLICATION NUMBER: 60/181,800
 14 <151> PRIOR FILING DATE: 2000-02-11
 16 <160> NUMBER OF SEQ ID NOS: 52
 18 <170> SOFTWARE: PatentIn version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1173
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (143)..(997)
 29 <400> SEQUENCE: 1
 30 gaattcggca cgagctgagg ggtgagccaa gccctgccat gtagtgcacg caggacatca      60
 32 acaaacacag ataacaggaa atgatccatt ccctgtggtc acttattcta aaggccccaa     120
 34 ccttcaaagt tcaagtagtg at atg gat gac tcc aca gaa agg gag cag tca      172
 35                         Met Asp Asp Ser Thr Glu Arg Glu Gln Ser
 36                         1               5                  10
 38 cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag gag      220
 39 Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys Glu
 40                 15                  20                  25
 42 tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc tcc      268
 43 Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser Ser
 44             30                  35                  40
 46 aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg tct      316
 47 Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser
 48         45                  50                  55
 50 tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa ggg      364
 51 Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly
 52     60                  65                  70
 54 gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag aag      412
 55 Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu Lys
 56 75                  80                  85                  90
 58 ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg gag gaa gct cca      460
 59 Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro
 60                 95                 100                 105
 62 gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga gaa      508
 63 Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu
 64             110                 115                 120
 66 ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt cca      556
 67 Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly Pro
 68         125                 130                 135
```

RAW SEQUENCE LISTING DATE: 03/07/2001
PATENT APPLICATION: US/09/779,050 TIME: 11:03:02

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

```
70 gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt gaa      604
71 Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu
72     140                 145                 150
74 aca cca act ata caa aaa gga tct tac aca ttt gtt cca tgg ctt ctc      652
75 Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu
76 155                 160                 165                 170
78 agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag aat aaa ata ttg      700
79 Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu
80                 175                 180                 185
82 gtc aaa gaa act ggt tac ttt ttt ata tat ggt cag gtt tta tat act      748
83 Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr
84             190                 195                 200
86 gat aag acc tac gcc atg gga cat cta att cag agg aag aag gtc cat      796
87 Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val His
88         205                 210                 215
90 gtc ttt ggg gat gaa ttg agt ctg gtg act ttg ttt cga tgt att caa      844
91 Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln
92     220                 225                 230
94 aat atg cct gaa aca cta ccc aat aat tcc tgc tat tca gct ggc att      892
95 Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile
96 235                 240                 245                 250
98 gca aaa ctg gaa gaa gga gat gaa ctc caa ctt gca ata cca aga gaa      940
99 Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu
100                255                 260                 265
102 aat gca caa ata tca ctg gat gga gat gtc aca ttt ttt ggt gca ttg      988
103 Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala Leu
104             270                 275                 280
106 aaa ctg ctg tgacctactt acaccatgtc tgtagctatt ttcctccctt            1037
107 Lys Leu Leu
108         285
110 tctctgtacc tctaagaaga aagaatctaa ctgaaaatac caaaaaaaaa aaaaaaaaaa   1097
112 aaaaaaaagt agttaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   1157
114 aaaaactcgg aggggg                                                  1173
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 285
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
122 <400> SEQUENCE: 2
124 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu
125 1               5                  10                  15
128 Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
129             20                  25                  30
132 Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
133         35                  40                  45
136 Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
137     50                  55                  60
140 Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
141 65                  70                  75                  80
144 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
```

RAW SEQUENCE LISTING DATE: 03/07/2001
PATENT APPLICATION: US/09/779,050 TIME: 11:03:02

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

```
145                 85                  90                  95
148 Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
149             100                 105                 110
152 Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
153         115                 120                 125
156 Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
157     130                 135                 140
160 Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
161 145                 150                 155                 160
164 Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
165                 165                 170                 175
168 Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
169             180                 185                 190
172 Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
173         195                 200                 205
176 Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu
177     210                 215                 220
180 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu
181 225                 230                 235                 240
184 Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly
185                 245                 250                 255
188 Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu
189             260                 265                 270
192 Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
193         275                 280                 285
196 <210> SEQ ID NO: 3
197 <211> LENGTH: 1139
198 <212> TYPE: DNA
199 <213> ORGANISM: Mus musculus
201 <220> FEATURE:
202 <221> NAME/KEY: CDS
203 <222> LOCATION: (52)..(978)
205 <400> SEQUENCE: 3
206 gaattcggca cgagctccaa aggcctagac cttcaaagtg ctcctcgtgg a atg gat      57
207                                                         Met Asp
208                                                         1
210 gag tct gca aag acc ctg cca cca ccg tgc ctc tgt ttt tgc tcc gag      105
211 Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys Ser Glu
212         5                   10                  15
214 aaa gga gaa gat atg aaa gtg gga tat gat ccc atc act ccg cag aag      153
215 Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro Gln Lys
216     20                  25                  30
218 gag gag ggt gcc tgg ttt ggg atc tgc agg gat gga agg ctg ctg gct      201
219 Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu Leu Ala
220 35                  40                  45                  50
222 gct acc ctc ctg ctg gcc ctg ttg tcc agc agt ttc aca gcg atg tcc      249
223 Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala Met Ser
224                 55                  60                  65
226 ttg tac cag ttg gct gcc ttg caa gca gac ctg atg aac ctg cgc atg      297
```

RAW SEQUENCE LISTING DATE: 03/07/2001
PATENT APPLICATION: US/09/779,050 TIME: 11:03:02

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

```
227 Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu Arg Met
228             70                  75                  80
230 gag ctg cag agc tac cga ggt tca gca aca cca gcc gcc gcg ggt gct      345
231 Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala Gly Ala
232         85                  90                  95
234 cca gag ttg acc gct gga gtc aaa ctc ctg aca ccg gca gct cct cga      393
235 Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala Pro Arg
236     100                 105                 110
238 ccc cac aac tcc agc cgc ggc cac agg aac aga cgc gct ttc cag gga      441
239 Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe Gln Gly
240 115                 120                 125                 130
242 cca gag gaa aca gaa caa gat gta gac ctc tca gct cct cct gca cca      489
243 Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro Ala Pro
244                 135                 140                 145
246 tgc ctg cct gga tgc cgc cat tct caa cat gat gat aat gga atg aac      537
247 Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly Met Asn
248             150                 155                 160
250 ctc aga aac atc att caa gac tgt ctg cag ctg att gca gac agc gac      585
251 Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Asp
252         165                 170                 175
254 acg ccg act ata cga aaa gga act tac aca ttt gtt cca tgg ctt ctc      633
255 Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp Leu Leu
256     180                 185                 190
258 agc ttt aaa aga gga aat gcc ttg gag gag aaa gag aac aaa ata gtg      681
259 Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys Ile Val
260 195                 200                 205                 210
262 gtg agg caa aca ggc tat ttc ttc atc tac agc cag gtt cta tac acg      729
263 Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu Tyr Thr
264                 215                 220                 225
266 gac ccc atc ttt gct atg ggt cat gtc atc cag agg aag aaa gta cac      777
267 Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys Val His
268             230                 235                 240
270 gtc ttt ggg gac gag ctg agc ctg gtg acc ctg ttc cga tgt att cag      825
271 Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile Gln
272         245                 250                 255
274 aat atg ccc aaa aca ctg ccc aac aat tcc tgc tac ttg gct ggc atc      873
275 Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Leu Ala Gly Ile
276     260                 265                 270
278 gcg agg ctg gaa gaa gga gat gag att cag ctt gca att cct cgg gag      921
279 Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro Arg Glu
280 275                 280                 285                 290
282 aat gca cag att tca cgc aac gga gac gac acc ttc ttt ggt gcc cta      969
283 Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly Ala Leu
284                 295                 300                 305
286 aaa ctg ctg taactcactt gctggagtgc gtgatcccct tccctcgtct             1018
287 Lys Leu Leu
290 tctctgtacc tccgagggag aaacagacga ctggaaaaat aaaagatggg gaaagccgtc   1078
292 agcgaaagtt ttctcgtgac ccgttgaatc tgatccaaac caggaaatat aacagacagc   1138
294 c                                                                  1139
```

RAW SEQUENCE LISTING DATE: 03/07/2001
PATENT APPLICATION: US/09/779,050 TIME: 11:03:02

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

297 <210> SEQ ID NO: 4
298 <211> LENGTH: 309
299 <212> TYPE: PRT
300 <213> ORGANISM: Mus musculus
302 <400> SEQUENCE: 4
304 Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys
305 1 5 10 15
308 Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
309 20 25 30
312 Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
313 35 40 45
316 Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
317 50 55 60
320 Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
321 65 70 75 80
324 Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
325 85 90 95
328 Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
329 100 105 110
332 Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
333 115 120 125
336 Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
337 130 135 140
340 Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
341 145 150 155 160
344 Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
345 165 170 175
348 Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp
349 180 185 190
352 Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys
353 195 200 205
356 Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu
357 210 215 220
360 Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys
361 225 230 235 240
364 Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys
365 245 250 255
368 Ile Gln Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Leu Ala
369 260 265 270
372 Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro
373 275 280 285
376 Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly
377 290 295 300
380 Ala Leu Lys Leu Leu
381 305
384 <210> SEQ ID NO: 5
385 <211> LENGTH: 278
386 <212> TYPE: PRT
387 <213> ORGANISM: Homo sapiens

09/779,050 6

(See item 6 on Error Summary Sheet)

<210> 5
<211> 278
<212> PRT
<213> Homo sapiens

This implies variable length, which is not permitted.

<220>
<221> misc feature
<223> X = one or more naturally occurring amino acid residues.

Xaa can only represent a single amino acid

<400> 5

Met Asp Xaa Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Cys
1 5 10 15

Xaa Xaa Lys Xaa Glu Xaa Met Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Gly Xaa Leu
35 40 45

Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Xaa Xaa Xaa Thr Xaa
50 55 60

Xaa Ser Xaa Tyr Gln Xaa Ala Ala Leu Gln Xaa Asp Leu Xaa Xaa Leu
65 70 75 80

Arg Xaa Glu Leu Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Ala Xaa Ala
85 90 95

Gly Ala Pro Xaa Xaa Thr Ala Gly Xaa Lys Xaa Xaa Xaa Pro Xaa Ala
100 105 110

Pro Xaa Xaa Xaa Asn Ser Ser Xaa Xaa Xaa Arg Asn Xaa Arg Ala Xaa
115 120 125

Gln Gly Pro Glu Glu Thr Xaa Xaa Gln Asp Cys Leu Gln Leu Ile Ala
130 135 140

Asp Ser Xaa Thr Pro Thr Ile Xaa Lys Gly Xaa Tyr Thr Phe Val Pro
145 150 155 160

Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn
165 170 175

Lys Ile Xaa Val Xaa Xaa Thr Gly Tyr Phe Phe Ile Tyr Xaa Gln Val
180 185 190

Leu Tyr Thr Asp Xaa Xaa Xaa Ala Met Gly His Xaa Ile Gln Arg Lys
195 200 205

Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg
210 215 220

Cys Ile Gln Asn Met Pro Xaa Thr Leu Pro Asn Asn Ser Cys Tyr Ser
225 230 235 240

(partial listing of Seq. 5)

Please ensure all sequences with this error are corrected.

FYI

Please Note:
Use of n and/or Xaa have b en detected in the Sequenc Listing. Please review the Sequence Listing to ensure that a corresp nding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 03/07/2001
PATENT APPLICATION: US/09/779,050 TIME: 11:03:03

Input Set : A:\A-570B.ST25 (US).txt
Output Set: N:\CRF3\03072001\I779050.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:396 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:396 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:399 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:402 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:405 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:408 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:411 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:414 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:417 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:420 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:423 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:429 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:432 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:438 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:441 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:444 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:462 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:462 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:465 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:468 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:471 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:474 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:477 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1156 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1156 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25
L:1159 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
M:340 Repeated in SeqNo=25
L:1177 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1177 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:26
L:1199 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1199 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27
L:1202 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
M:340 Repeated in SeqNo=27
L:1205 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1208 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1211 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1217 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1220 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:1223 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27